I. AMENDMENT

Listing of Claims:

The following listing of claims replaces all previous listings or versions thereof:

1.-53. (Cancelled)

54. (Previously presented) A method for depleting rRNA from a sample comprising:

a) incubating the sample with at least a first (1) bridging oligonucleotide comprising a bridging region comprising a poly-purine region of at least 5 residues and a targeting region comprising at least 5 contiguous nucleic acid residues complementary to a sequence of an rRNA molecule and a (2) capture oligonucleotide comprising a magnetic bead and a capture region comprising a poly-pyrimidine region of at least 5 residues, under conditions to allow hybridization between the bridging oligonucleotide and the capture oligonucleotide and the bridging oligonucleotide and the rRNA;

b) incubating the sample with a magnetic bead;

c) isolating the magnetic bead; and,

d) discarding the magnetic bead with the rRNA.

55.-82. (Cancelled)

83. (Previously Presented) A method for depleting or isolating a targeted rRNA from a sample comprising:

a) obtaining a kit comprising: a capture oligonucleotide comprising a capture region and a magnetic bead; and at least a first bridging oligonucleotide comprising (1) at least one bridging region complementary to all or part of the capture region of the capture oligonucleotide and a (2) at least one targeting region comprising 10 contiguous nucleic acids complementary to a sequence of an rRNA;

b) incubating the sample with the bridging oligonucleotide under conditions allowing hybridization between the targeting region and the targeted rRNA;

c) incubating the bridging oligonucleotide with the capture oligonucleotide under conditions allowing hybridization between the bridging region and the capture region; and

d) isolating the targeted rRNA from the remainder of the sample by incubating the sample with a magnetic field.

84. (Original) The method of claim 83, further comprising:

e) obtaining the remainder of the sample enriched for mRNA;

f) preparing cDNA from the mRNA.

85. (Original) The method of claim 84, further comprising:

g) constructing a nucleic acid array with the cDNA.

86.-90. (Cancelled)

91. (New) The method of claim 54, wherein the rRNA is prokaryotic 16S, prokaryotic 23S, eukaryotic 17S or 18S, or eukaryotic 28S rRNA.

92. (New) The method of claim 91, wherein the rRNA comprises the sequence of SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:72, or SEQ ID NO:73.

93. (New) The method of claim 54, wherein the sample comprises eukaryotic nucleic acid.

94. (New) The method of claim 54, wherein the sample comprises prokaryotic nucleic acid.

95. (New) The method of claim 93, wherein the sample comprises eukaryotic and prokaryotic nucleic acids.

96. (New) The method of claim 94, wherein the prokaryotic nucleic acid is from a gram positive bacterium.

97. (New) The method of claim 94, wherein the prokaryotic nucleic acid is from a gram negative bacterium.

98. (New) The method of claim 54, wherein the bridging region, targeting region, or capture region comprises at least 10 nucleic acid residues.

99. (New) The method of claim 98, wherein the bridging region, targeting region, or capture region comprises at least 15 nucleic acid residues.

100. (New) The method of claim 99, wherein the bridging region, targeting region, or capture region comprises at least 20 nucleic acid residues.

101. (New) The method of claim 54, further comprising incubating the sample with a second bridging oligonucleotide comprising (1) at least one bridging region comprising at least 5 nucleic acid residues and (2) at least one targeting region comprising at least 5 nucleic acid residues, under conditions allowing hybridization between the targeting region of the second bridging oligonucleotide and the targeted nucleic acid.

102. (New) The method of claim 101, wherein the targeting region of the first bridging oligonucleotide is complementary to the sequence of a targeted nucleic acid and the targeting region of the second bridging oligonucleotide is complementary to a different sequence of a targeted nucleic acid.

103. (New) The method of claim 102, wherein the targeting region of the first bridging oligonucleotide and the targeting region of the second bridging oligonucleotide are complementary to the same targeted nucleic acid.

104. (New) The method of claim 102, wherein the targeting region of the first bridging oligonucleotide and the targeting region of the second bridging oligonucleotide are complementary to different targeted nucleic acids.

105. (New) The method of claim 104, wherein the targeting region of the first bridging oligonucleotide is complementary to a sequence of the largest rRNA molecule and the targeting region of the second bridging oligonucleotide is complementary to a sequence of the second largest rRNA molecule in the sample.

106. (New) The method of claim 101, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 100 and 5000 residues of the 5' or 3' end of the targeted nucleic acid.

107. (New) The method of claim 106, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 200 and 3000 residues of the 5' or 3' end of the targeted nucleic acid.

108. (New) The method of claim 107, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 300 and 1500 residues of the 5' or 3' end of the targeted nucleic acid.

109. (New) The method of claim 108, wherein targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 400 and 900 residues of the 5' or 3' end of the targeted nucleic acid.

110. (New) The method of claim 109, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 500 and 700 residues of the 5' or 3' end of the targeted nucleic acid.

111. (New) The method of claim 101, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence at the 3' or 5' end of the targeted nucleic acid.

112. (New) The method of claim 101, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence not within 100 residues from the 3' or 5' end of the targeted nucleic acid.

113. (New) The method of claim 101, wherein targeting region of the first or second bridging oligonucleotide hybridizes to a sequence not within 200 residues from the 3' or 5' end of the targeted nucleic acid.

114. (New) The method of claim 101, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence not within 400 residues from the 3' or 5' ends of the targeted nucleic acid.

115. (New) The method of claim 101, wherein the targeting region of the first or second bridging oligonucleotide comprises SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, or SEQ ID NO:22.

116. (New) The method of claim 54, wherein the bridging oligonucleotide comprises a second targeting region comprising at least 5 nucleic acid residues complementary to a different sequence than the sequence to which the first targeting region is complementary.

117. (New) The method of claim 116, wherein the first targeting region is complementary to a different targeted nucleic acid than the second targeting region is.

118. (New) The method of claim 54, wherein the first bridging oligonucleotide comprises two bridging regions.

119. (New) The method of claim 54, wherein the bridging oligonucleotide or the capture oligonucleotide is RNA, DNA, LNA, iso-bases, or a peptide nucleic acid.

120. (New) The method of claim 54, further comprising washing the capture oligonucleotide after incubation with the sample and the bridging oligonucleotide.

121. (New) The method of claim 54, wherein a) and b) are performed at the same temperature.

122. (New) The method of claim 54, wherein a) and b) are performed at a different temperature.

123. (New) The method of claim 54, wherein a) and b) are performed at the same time.

124. (New) The method of claim 54, wherein isolating the magnetic bead comprises exposing the sample with the capture oligonucleotide to a magnetic field.

125. (New) The method of claim 54, wherein the sample, capture oligonucleotide, and bridging oligonucleotide are incubated in a buffer comprising TMAC or TEAC.

126. (New) The method of claim 54, further comprising:

d) producing cDNA using mRNA in the remainder of the sample.

127. (New) The method of claim 130, further comprising:

e) contacting a nucleic acid array with the cDNA.

128. (new) The method of claim 54, wherein the targeted nucleic acid is depleted by at least 50% in the sample.

129. (new) The method of claim 128, wherein the targeted nucleic acid is depleted by at least 60% in the sample.

130. (new) The method of claim 129, wherein the targeted nucleic acid is depleted by at least 70% in the sample.

131. (new) The method of claim 130, wherein the targeted nucleic acid is depleted by at least 80% in the sample.

132. (new) The method of claim 54, further comprising isolating the nontargeted nucleic acid in the depleted sample.

133. (New) The method of claim 83, wherein the rRNA is prokaryotic 16S, prokaryotic 23S, eukaryotic 17S or 18S, or eukaryotic 28S rRNA.

134. (New) The method of claim 133, wherein the rRNA comprises the sequence of SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ

ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:72, or SEQ ID NO:73.

135. (New) The method of claim 83, wherein the sample comprises eukaryotic nucleic acid.

136. (New) The method of claim 83, wherein the sample comprises prokaryotic nucleic acid.

137. (New) The method of claim 135, wherein the sample comprises eukaryotic and prokaryotic nucleic acids.

138. (New) The method of claim 136, wherein the prokaryotic nucleic acid is from a gram positive bacterium.

139. (New) The method of claim 136, wherein the prokaryotic nucleic acid is from a gram negative bacterium.

140. (New) The method of claim 83, wherein the bridging region, targeting region, or capture region comprises at least 10 nucleic acid residues.

141. (New) The method of claim 140, wherein the bridging region, targeting region, or capture region comprises at least 15 nucleic acid residues.

142. (New) The method of claim 141, wherein the bridging region, targeting region, or capture region comprises at least 20 nucleic acid residues.

143. (New) The method of claim 83, wherein the bridging region or the capture region is polypurine or polypyrimidine.

144. (New) The method of claim 143, wherein the bridging region is polypurine and the capture region is polypyrimidine.

145. (New) The method of claim 83, further comprising incubating the sample with a second bridging oligonucleotide comprising (1) at least one bridging region comprising at least 5 nucleic acid residues and (2) at least one targeting region comprising at least 5 nucleic acid residues, under conditions allowing hybridization between the targeting region of the second bridging oligonucleotide and the targeted nucleic acid.

146. (New) The method of claim 145, wherein the targeting region of the first bridging oligonucleotide is complementary to the sequence of a targeted nucleic acid and the targeting region of the second bridging oligonucleotide is complementary to a different sequence of a targeted nucleic acid.

147. (New) The method of claim 146, wherein the targeting region of the first bridging oligonucleotide and the targeting region of the second bridging oligonucleotide are complementary to the same targeted nucleic acid.

148. (New) The method of claim 146, wherein the targeting region of the first bridging oligonucleotide and the targeting region of the second bridging oligonucleotide are complementary to different targeted nucleic acids.

149. (New) The method of claim 148, wherein the targeting region of the first bridging oligonucleotide is complementary to a sequence of the largest rRNA molecule and the targeting region of the second bridging oligonucleotide is complementary to a sequence of the second largest rRNA molecule in the sample.

150. (New) The method of claim 145, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 100 and 5000 residues of the 5' or 3' end of the targeted nucleic acid.

151. (New) The method of claim 150, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 200 and 3000 residues of the 5' or 3' end of the targeted nucleic acid.

152. (New) The method of claim 151, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 300 and 1500 residues of the 5' or 3' end of the targeted nucleic acid.

153. (New) The method of claim 152, wherein targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 400 and 900 residues of the 5' or 3' end of the targeted nucleic acid.

154. (New) The method of claim 153, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 500 and 700 residues of the 5' or 3' end of the targeted nucleic acid.

155. (New) The method of claim 145, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence at the 3' or 5' end of the targeted nucleic acid.

156. (New) The method of claim 145, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence not within 100 residues from the 3' or 5' end of the targeted nucleic acid.

157. (New) The method of claim 145, wherein targeting region of the first or second bridging oligonucleotide hybridizes to a sequence not within 200 residues from the 3' or 5' end of the targeted nucleic acid.

158. (New) The method of claim 145, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence not within 400 residues from the 3' or 5' ends of the targeted nucleic acid.

159. (New) The method of claim 145, wherein the targeting region of the first or second bridging oligonucleotide comprises SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10,

SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, or SEQ ID NO:22.

160. (New) The method of claim 83, wherein the bridging oligonucleotide comprises a second targeting region comprising at least 5 nucleic acid residues complementary to a different sequence than the sequence to which the first targeting region is complementary.

161. (New) The method of claim 160, wherein the first targeting region is complementary to a different targeted nucleic acid than the second targeting region is.

162. (New) The method of claim 83, wherein the first bridging oligonucleotide comprises two bridging regions.

163. (New) The method of claim 83, wherein the bridging oligonucleotide or the capture oligonucleotide is RNA, DNA, LNA, iso-bases, or a peptide nucleic acid.

164. (New) The method of claim 83, further comprising washing the capture oligonucleotide after incubation with the sample and the bridging oligonucleotide.

165. (New) The method of claim 83, wherein a) and b) are performed at the same temperature.

166. (New) The method of claim 83, wherein a) and b) are performed at a different temperature.

167. (New) The method of claim 165, wherein a) and b) are performed at the same time.

168. (New) The method of claim 83, wherein isolating the targeted nucleic acid away from the sample comprises exposing the sample with the capture oligonucleotide to a magnetic field.

169. (New) The method of claim 83, wherein the sample, capture oligonucleotide, and bridging oligonucleotide are incubated in a buffer comprising TMAC or TEAC.

170. (New) The method of claim 84, further comprising:

g) contacting a nucleic acid array with the cDNA.

171. (New) The method of claim 83, wherein the targeted nucleic acid is depleted by at least 50% in the sample.

172. (New) The method of claim 171, wherein the targeted nucleic acid is depleted by at least 60% in the sample.

173. (New) The method of claim 172, wherein the targeted nucleic acid is depleted by at least 70% in the sample.

174. (New) The method of claim 83, wherein the targeted nucleic acid is depleted by at least 80% in the sample.

175. (New) The method of claim 83, further comprising isolating the nontargeted nucleic acid in the depleted sample.